Am ndment

Amendments to the Specification:

Page 1 from line 6 to 10, please delete the paragraph in the specification and insert the following paragraph:

This application is a continuation of Application No. 08/948, 958, filed October 10, 1997, which claims the benefit of Provisional Application No. 60/028, 687, filed October 18, 1996.

Please replace the paragraph beginning at page 20, line 18, with the following paragraph:

- - Fig. 4A-D shows the amino acid sequence of human IL-12 p40 subunit (SEQ ID NO: 1), along with the codons which can code for each of the amino acid.

Please replace the paragraph beginning at page 20, line 21, with the following paragraph:

- - Fig. 5A-C shows the amino acid sequence of human IL-12 p35 subunit (SEQ ID NO: 5), along with the codons which can code for each of the amino acids.

Page 8, line 23, please change "Initally" to - - - initially - - -.

Page 31, line 27, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 32, line 17, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 32, line 30, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 33, line 5, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 33, line 18, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 34, line 3, please change "OPTIVS8B" to - - - OPTIVS8 - - -.

Page 30, line 6, at the beginning of the line, please insert - - SEQ ID NO: 9 - -

Page 32, line 12, at the beginning of the line, please insert - - SEQ ID NO: 10 - -

Page 37, line 20, at the beginning of the line, please insert - - SEQ ID NO:12 - -

Please replace the paragraph beginning at page 30, line 24 to page 31, line 3, with the following paragraph:

- - The sequence of the synthetic 5'UTR was designed to be moderate in length (54 nucleotides (nts)) (SEQ ID NO: 9 residues # 1 through # 54), to be deficient in G but rich in C and A residues, to lack an upstream ATG, to place the intended ATG within the context of a optimal Kozak sequence (CCACCATGG) (SEQ ID NO: 9 residues # 50 through 58), and to lack potential secondary structure. The synthetic 5' UTR sequence was also designed to lack AU-rich sequences that target mRNAs to be rapidly degraded in the cytoplasm.

Please insert "SEQ ID NO:10 residues from #1 through #15 for CAGGTAAAGTGTCTTC and SEQ ID NO:10 residues from #16 through #45 for TACTAACGGTTCTTTTTTTCTCTTCACAGG" at the beginning of line 10, page 32.

Please replace the paragraph beginning at page 33, line 13, with the following paragraph:

- - The sequence of the 3' splice site (3'ss) matches the established consensus sequence, Y_{11}NYAG↓G (SEQ ID NO: 11), where Y=C or T, and N = any base. In 3' splice sites, the polypyrimidine tract (Y_{11}) is the major determinant of splice site strength. For optimal splice site function in OPTIVS8, the length of the polypyrimidine tract was extended to 16 bases, and its sequence was adjusted to contain 7 consecutive T residues. This features was included because Roscigno et al., 1993, J. Biol. Chem. 268:11222-11229, demonstrated that optimal splicing requires the presence of at least 5 consecutive T residues in the polypyrimidine tract.